

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:20:10 ; Search time 52.2 Seconds

(without alignments)
36.422 Million cell updates/sec

Title: US-09-331-631A-32

Perfect score: 76

Sequence: 1 CXXCXXCXXXXXXXXXXCXXCXXC 28

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_66:**
2: PIR1:**
3: PIR2:**
4: PIR3:**
4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	74	2 S25773	testis-specific pr
2	76	100.0	152	2 T18975	hypothetical prote
3	76	100.0	164	2 T24272	hypothetical prote
4	76	100.0	188	2 T15651	hypothetical prote
5	67	88.2	55	2 S25774	testis-specific pr
6	67	88.2	57	1 SMKD2S	metallochionein 2
7	67	88.2	57	2 S59073	metallochionein is
8	67	88.2	58	1 SMKD1S	metallochionein 1
9	67	88.2	58	2 S59072	metallochionein 1
10	67	88.2	58	2 A37039	metallochionein 1
11	67	88.2	63	2 S43567	testis-specific pr
12	67	88.2	63	2 S25772	testis-specific pr
13	67	88.2	68	2 S25775	keratin I, feather
14	67	88.2	98	1 KRCHFI	keratin II, feathe
15	67	88.2	98	1 KRCHFI	keratin II, feathe
16	67	88.2	98	2 S06807	keratin, feather (
17	67	88.2	98	2 S06806	keratin, feather (
18	67	88.2	98	2 S06808	keratin, feather (
19	67	88.2	118	2 S26889	hypothetical prote
20	67	88.2	154	2 T17816	hypothetical prote
21	67	88.2	157	1 W5MR1	E5 protein - thesu
22	67	88.2	178	2 A23219	high-cysteine chor
23	67	88.2	223	2 B38346	ultra-high-sulfur
24	67	88.2	230	2 A38346	ultra-high-sulfur
25	67	88.2	247	2 I48699	outer dense fiber
26	67	88.2	248	2 E71602	probable integral
27	67	88.2	260	2 T17638	glycine tyrosine-r
28	67	88.2	272	2 T36770	probable expressio
29	67	88.2	273	2 T16246	hypothetical prote

30	67	88.2	329	2 A48805	insulin-like growt
31	67	88.2	330	2 T25169	hypothetical prote
32	67	88.2	341	2 T29598	hypothetical prote
33	67	88.2	408	2 B71272	hypothetical prote
34	67	88.2	654	2 T30136	hypothetical prote
35	67	88.2	728	2 T45617	diacylglycerol kin
36	67	88.2	780	2 S71467	diacylglycerol kin
37	67	88.2	782	2 A34102	von Willebrand fac
38	67	88.2	802	2 T24293	hypothetical prote
39	67	88.2	915	2 T21772	hypothetical prote
40	67	88.2	927	2 T21772	hypothetical prote
41	67	88.2	949	2 T24294	hypothetical prote
42	67	88.2	955	2 T18435	hypothetical prote
43	67	88.2	1023	2 T30257	IgG Fc binding pro
44	67	88.2	1133	1 S41478	dna repair protein
45	67	88.2	1255	1 A24571	protein-tyrosine k

ALIGNMENTS

RESULT 1
S25773
testis-specific protein Mst84Db - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C:Accession: S25773; B56565
R:Kuhn, R.; Kuhn, C.; Boersch, D.; Gaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991
A:Title: A cluster of four genes selectively expressed in the male germ line of Dros
A:Reference number: A56565; M0ID:92102953
A:Accession: S25773
A:Molecule type: DNA
A:Residues: 1-74 <KUH>
A:Cross-references: EMBL:X67703; NID:q11072; PIDD:CAA47938.1; PIDD:q11074
A:Note: Sequence extracted from NCBI backbone (NCBIN:74217, NCBIIP:74220)
C:Genetics:
A:Gene: Mst84Db
A:Cross-references: FlyBase:FBgn0004173
A:Map position: 3
C:Superfamily: fruit fly testis-specific protein
C:Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 76; DB 2; Length 74;
Best Local Similarity 21.4%; Pred. No. 20;
Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXCXXXXXXXXXXCXXCXXC 28
Db 12 CSPCGGCGPCGCGCGCGSCGSCGSCGSCGSC 39

RESULT 2
T18975
hypothetical protein C06A1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18975
R:McMurray, A.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19054
A:Accession: T18975
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-152 <WIL>
A:Cross-references: EMBL:Z49886; PIDD:CAA90055.1; GSPDB:GN00020; CESP:C06A1.6
A:Experimental source: clone C06A1
C:Genetics:
A:Gene: CESP:C06A1.6
A:Map position: 2
A:Introns: 22/3

